WEST Search History

DATE: Tuesday, December 24, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,DWPI; PLUR=YES; OP=ADJ			
L1	kit same (single near (container or tube)) same primer same deoxynucleotide triphosphate	0	L1
L2	kit and (single near (container or tube)) and primer and deoxynucleotide triphosphate	44	L2
L3	L2 and sequenc$	44	L3
L4	L3 and ((sense and antisense strand) near primer)	1	L4
L5	primer near (sense and antisense strand)	22	L5
L6	L5 and kit	18	L6
L7	L6 and sequenc$	18	L7
L8	L7 and (single tube or container)	0	L8
L9	l7 and container	0	L9
L10	L7 and tube	12	L10
L11	L10 and genomic or l10 and microorganism DNA	12	L11
L12	L11 and four deoxynucleotide triphosphates	0	L12
L13	L11 and deoxynucleotide triphosphate	1	L13
L14	L12 and dideoxynucleotide triphosphate	0	L14
L15	L11 and didexynucleotide triphosphate	0	L15
L16	L11 and dideoxynucleotide triphosphate	0	L16
L17	L11 and polymerase	12	L17
DB=USPT,DWPI; PLUR=YES; OP=ADJ			
L18	6214555.pn. or 6083699.pn. or 5789168.pn. or 5830657.pn. or 5888736.pn.	9	L18

END OF SEARCH HISTORY

WEST

Generate Collection Print

L18: Entry 3 of 9 File: USPT Mar 30, 1999

US-PAT-NO: 5888736
DOCUMENT-IDENTIFIER: US 5888736 A

TITLE: Method, compositions and kit for detection and identification of microorganisms

DATE-ISSUED: March 30, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lacroix; Jean-Michel	Etobicoke			CA
Leushner; James	North York			CA
Hui; May	Toronto			CA
Dunn; James M.	Scarborough			CA
Larson; Marina T.	Yorktown	NY		

US-CL-CURRENT: 435/6; 435/91.2

CLAIMS:

We claim:

1. A method for evaluating a natural abundance sample for the presence of a target DNA sequence from a target microorganism, said natural abundance sample containing the target DNA sequence substantially without preferential amplification of the target DNA sequence relative to non-target DNA sequences in the sample, comprising the steps of:

(a) combining the natural abundance sample directly and in a single reaction mixture with first and second primers, a nucleotide triphosphate feedstock mixture, a chain-terminating nucleotide triphosphate and a thermally stable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides in an amplification mixture, said first and second primers binding to the sense and antisense strands, respectively, and flanking the target DNA sequence within the target microorganism genome, and at least one of said first and second primers being labeled with a fluorescent label;

(b) exposing the reaction mixture to a plurality of temperature cycles each of which includes at least a high temperature denaturation phase and a lower temperature extension phase, thereby producing a plurality of species of terminated fragments if DNA from the target microorganism is present in the natural abundance sample, each species of terminated fragment corresponding to a different incorporation position for the chain-terminating nucleotide triphosphate in the DNA of the target microorganism DNA;

(c) evaluating the terminated fragments produced to determine the incorporation positions of the chain-terminating nucleotide triphosphate; and

(d) comparing the incorporation positions of the chain-terminating nucleotide triphosphate to the target DNA sequence to determine if the target DNA sequence is present in the sample.

2. The method of claim 1, wherein the first and second primers are each labeled with a different fluorescent label.

3. The method of claim 1, wherein the chain terminating nucleotide triphosphate is present in a mole ratio to the corresponding nucleotide triphosphate of from 1:50 to 1:1000.

4. The method of claim 3, wherein the mole ratio of the chain terminating nucleotide triphosphate to the corresponding nucleotide triphosphate is from 1:100 to 1:500.

5. The method according to claim 1, wherein the target microorganism is Chlamydia trachomatis.

6. The method according to claim 5, wherein the first and second primers are selected from among the group consisting of the oligonucleotides given by Seq. ID. Nos. 1-17.

7. The method according to claim 1, wherein the target microorganism is human immunodeficiency virus.

8. The method according to claim 7, wherein the first and second primers are selected from among the group consisting of the oligonucleotides given by Seq. ID. Nos. 18-20.

9. The method according to claim 1, wherein the target microorganism is human papilloma virus.

10. The method according to claim 9, wherein the first and second primers are selected from among the group consisting of the oligonucleotides given by Seq. ID. Nos.21-22.

11. A method for evaluating a natural abundance sample for the presence of a target DNA sequence from a target microorganism, said natural abundance sample containing the target DNA sequence substantially without preferential amplification of the target DNA sequence relative to non-target DNA sequences in the sample, comprising the steps of:

(a) combining each of from one to three aliquots of the natural abundance sample directly and in a single reaction mixture with first and second primers, a nucleotide triphosphate feedstock mixture, a single chain-terminating nucleotide triphosphate and a thermally stable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides in an amplification mixture to form a reaction mixture, said first and second primers binding to the sense and antisense strands, respectively, and flanking the target DNA sequence within the target microorganism genome, and at least one of said first and second primers being labeled with a fluorescent label, wherein the chain-terminating nucleotide triphosphate added to each aliquot is different from that added to the other aliquots;

(b) exposing the reaction mixture to a plurality of temperature cycles each of which includes at least a high temperature denaturation phase and a lower temperature extension phase, thereby producing a plurality of species of terminated fragments if DNA from the target microorganism is present in the natural abundance sample, each species of terminated fragment corresponding to a different incorporation position for the chain-terminating nucleotide triphosphate in the DNA of the target microorganism DNA;

(c) evaluating the terminated fragments produced to determine the incorporation positions of the chain-terminating nucleotide triphosphate; and

(d) comparing the incorporation positions of the chain-terminating nucleotide triphosphate to the target DNA sequence to determine if the target DNA sequence is present in the sample.

L18: Entry 5 of 9 File: USPT Aug 4, 1998

US-PAT-NO: 5789168
DOCUMENT-IDENTIFIER: US 5789168 A

TITLE: Method for amplification and sequencing of nucleic acid polymers

DATE-ISSUED: August 4, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Leushner; James	North York			CA
Hui; May	Toronto			CA
Dunn; James M.	Scarborough			CA
Larson; Marina T.	Yorktown	NY		

US-CL-CURRENT: 435/6; 435/91.2

CLAIMS:

We claim:

1. A method for analyzing a nucleic acid-containing sample comprising the steps of:

performing a multiplex amplification reaction on the nucleic acid-containing sample using a plurality of amplification primers pairs, one pair for each of a plurality of regions to be analyzed, to produce a mixture of amplified fragments, one species of amplified fragment for each of the plurality of regions to be analyzed; and

determining the sequence of at least one of the species of amplified fragments, wherein the sequence is determined by combining the mixture of amplified fragments produced in the multiplex amplification reaction directly with a sequencing reaction mixture for the production of sequencing fragments and evaluating the sequencing fragments produced therefrom.

2. The method of claim 1, wherein at least one aliquot of the mixture of amplified fragments produced in the multiplex amplification reaction is combined with a sequencing mixture comprising

first and second sequencing primers,

a nucleotide triphosphate feedstock mixture,

a chain-terminating nucleotide triphosphate, and

a thermally stable polymerase enzyme which incorporates dideoxynucleotide triphosphates into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotide triphosphates to form a sequencing reaction mixture, said first and second sequencing primers binding to the sense and antisense strands, respectively, of the amplified fragments from a selected one of the regions; and wherein the sequencing reaction mixture is exposed to a plurality of temperature cycles each of which includes at least a

high temperature denaturation phase and a lower temperature extension phase, thereby producing a plurality of terminated fragments; and that the terminated fragments are evaluated to determine the position of the base corresponding to the chain-terminating nucleotide triphosphate within the selected fragment.

3. The method according to claim 2, wherein at least one primer of each pair of amplification primers used in the multiplex amplification reaction is labeled with a capturable label, and wherein the amplified fragments are captured on a solid support and washed prior to combining them with the sequencing mixture.

4. The method according to claim 3, wherein the capturable label is biotin.

5. The method according claim 2, wherein the thermostable polymerase enzyme is THERMO SEQUENASE.TM..

6. The method according to claim 2, wherein at least one of the first and second sequencing primers in the sequencing mixture is labeled with a fluorescent label.

7. The method according to claim 2, wherein the first and second sequencing primers in the sequencing mixture are each labeled with a different spectroscopically-distinguishable fluorescent label.

8. The method according to claim 1, wherein the species of amplified fragments produced by the pairs of amplification primers each have a different length.

L18: Entry 4 of 9 File: USPT Nov 3, 1998

US-PAT-NO: 5830657
DOCUMENT-IDENTIFIER: US 5830657 A

TITLE: Method for single-tube sequencing of nucleic acid polymers

DATE-ISSUED: November 3, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Leushner; James	North York			CA
Hui; May	West Toronto			CA
Dunn; James M.	Scarborough			CA
Larson; Marina T.	Yorktown	NY		

US-CL-CURRENT: 435/6; 435/91.2, 536/24.3

CLAIMS:

We claim:

1. A method for sequencing of a selected region of a target nucleic acid polymer in a sample containing the selected region in substantially natural relative abundance, comprising the steps of:

(a) combining the sample containing the target region in substantially natural relative abundance with first and second primers, a nucleotide triphosphate feedstock mixture, a chain-terminating nucleotide triphosphate and a thermally stable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides in an amplification mixture to form a reaction mixture, said first and second primers binding to the sense and antisense strands, respectively, of the target nucleic acid polymer at locations flanking the selected region;

(b) exposing the reaction mixture to a plurality of temperature cycles each of which includes at least a high temperature denaturation phase and a lower temperature extension phase, thereby producing a plurality of terminated fragments; and

(c) evaluating terminated fragments produced during the additional cycles to determine the sequence of the selected region, wherein at least one of the first and second primers is labeled with a fluorescent label.

2. The method of claim 1, wherein the polymerase enzyme is THERMO SEQUENASE.TM..

3. The method of claim 1, wherein the first and second primers are each labeled with a different fluorescent label.

4. The method of claim 1, wherein the mole ratio of the dideoxynucleotide triphosphate to the corresponding deoxynucleotide triphosphate is from 1:50 to 1:500.

5. The method of claim 1, wherein the mole ratio of the dideoxynucleotide triphosphate to the corresponding deoxynucleotide triphosphate is from 1:100 to 1:300.

6. A kit for sequencing a plurality of DNA regions from a genomic DNA sample consisting of, in packaged combination, a single region-specific reagent for each DNA region, and optionally one or more non-region-specific reagents.

7. The kit according to claim 6, wherein the kit includes a polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides.

8. The kit according to claim 7, wherein the polymerase enzyme in THERMO SEQUENASE.TM..

L18: Entry 1 of 9 File: USPT Apr 10, 2001

US-PAT-NO: 6214555
DOCUMENT-IDENTIFIER: US 6214555 B1

TITLE: Method compositions and kit for detection

DATE-ISSUED: April 10, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Leushner; James	North York			CA
Hui; May	Toronto			CA
Dunn; James M.	Scarborough			CA
LaCroix; Jean-Michel	Etobicoke			CA

US-CL-CURRENT: 435/6; 530/350

CLAIMS:

We claim:

1. A composition comprising a mixture of four deoxynucleotide triphosphates and at least one dideoxynucleotide triphosphate corresponding to one of the four deoxynucleotide triphosphates, wherein the dideoxynucleotide triphosphate is present in a mole ratio to the corresponding deoxynucleotide triphosphate of from 1:50 to 1:500, said composition further comprising a thermally stable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides.

2. The composition according to claim 1, wherein the mole ratio is from 1:100 to 1:300.

3. A kit for detection of a target microorganism comprising, in packaged combination,

(a) a pair of primers which bind to the sense and antisense strands, respectively, and flank a selected region within the genome target microorganism; and

(b) a mixture of four deoxynucleotide triphosphates and at least dideoxynucleotide triphosphate corresponding to one of the four deoxynucleotide triphosphates, wherein the dideoxynucleotide triphosphate is present in a mole ratio to the corresponding deoxynucleotide triphosphate of from 1:50 to 1:1000.

(c) a polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides.

4. The kit according to claim 3, wherein the mole ratio is from 1:100 to 1:500.

5. The kit according to claim 3, wherein at least one of the primers is labeled with a fluorescent label.

6. The kit according to claim 3, wherein the primers are each labeled with a spectroscopically-distinct fluorescent label.

7. The kit according to claim 3, wherein the target microorganism is Chlamydia trachomatis.

8. The kit according to claim 7, wherein the first and second primers are selected from the group consisting of the oligonucleotides given by Seq. ID Nos. 1-17.

9. The kit according to claim 3, wherein the target microorganism is human immunodeficiency virus.

10. The kit according to claim 9, wherein the first and second primers are selected from the group consisting of the oligonucleotides given by Seq. ID Nos. 18-20.

11. The kit according to claim 3, wherein the target microorganism is human papilloma virus.

12. The kit according to claim 11, wherein the first and second primers are selected from the group consisting of the oligonucleotides given by Seq. ID Nos. 21-22.

L18: Entry 2 of 9 File: USPT Jul 4, 2000

US-PAT-NO: 6083699
DOCUMENT-IDENTIFIER: US 6083699 A

TITLE: Method for bi-directional sequencing of nucleic acid polymers

DATE-ISSUED: July 4, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Leushner; James	North York			CA
Hui; May	West Toronto			CA
Dunn; James M.	Scarborough			CA
Larson; Marina T.	Yorktown	NY		
Lacroix; Jean-Michel	Etobicoke			CA
Shipman; Robert	Mississauga			CA

US-CL-CURRENT: 435/6

CLAIMS:

We claim:

1. A method for simultaneously determining the positions of a selected nucleotide base in a target region of both strands of a denatured duplex nucleic acid polymer comprising the steps of:

(a) combining the nucleic acid polymer with a reactant mixture comprising

first and second oligonucleotide primers, said primers binding to the sense and antisense strands, respectively, of the nucleic acid polymer at a location flanking the target region,

a thermostable DNA polymerase,

a chain-terminating nucleotide triphosphate complementary to the selected nucleotide base, and

reagents for synthesis of chain extension products to form a reaction mixture;

(b) processing the reaction mixture through a plurality of thermal cycles, each including at least a chain extension phase and a denaturation phase to produce chain extension products;

(c) evaluating the chain extension products to determine the positions of the selected bases, wherein the first and second oligonucleotide primers are each labeled with different, spectroscopically distinguishable fluorescent labels.

2. The method according to claim 1, wherein the reaction mixture comprises a thermally-stable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides.

3. The method according to claim 2, wherein the sample is a natural abundance sample which has not been subjected to a preferential purification or amplification step to increase the amount of target DNA relative to non-target DNA present in the initial sample.

4. The method of claim 2, wherein the mole ratio of the dideoxynucleotide triphosphate to the corresponding deoxynucleotide triphosphate in the reaction mixture is from 1:50 to 1:1000.

5. The method of claim 4, wherein the mole ratio of the dideoxynucleotide triphosphate to the corresponding deoxynucleotide triphosphate is from 1:100 to 1:300.